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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=7; day=2; hr=8; min=17; sec=5; ms=90; ]

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Reviewer Comments:

1.

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 9 )

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 10 )

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 11 )

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 12 )

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 13 )

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 14 )

E249                   Order Sequence Error <211> -> <213>; Expected Mandatory  
Tag: <212> in SEQID ( 15 )

E250                   Structural Validation Error; Sequence listing may not be  
indexable

<210>   9

<211>   527

<213>   unknown

<220>

<223>   protein p12 of T2 phage

\* \* \* \* \*

For SEQ ID # 9 through 15, numeric identifier "<212> Type" is mandatory.  
Please insert numeric identifier <212>, with the appropriate response,  
between numeric identifiers <211> and <213> for each SEQ ID # 9 through

15.

2.

W213	Artificial or Unknown found in <213> in SEQ ID (1)
W213	Artificial or Unknown found in <213> in SEQ ID (2)
W213	Artificial or Unknown found in <213> in SEQ ID (3)
W213	Artificial or Unknown found in <213> in SEQ ID (4)
W213	Artificial or Unknown found in <213> in SEQ ID (5)
W213	Artificial or Unknown found in <213> in SEQ ID (6)
W213	Artificial or Unknown found in <213> in SEQ ID (7)
W213	Artificial or Unknown found in <213> in SEQ ID (8)
W213	Artificial or Unknown found in <213> in SEQ ID (9)
W213	Artificial or Unknown found in <213> in SEQ ID (10)
W213	Artificial or Unknown found in <213> in SEQ ID (11)
W213	Artificial or Unknown found in <213> in SEQ ID (12)
W213	Artificial or Unknown found in <213> in SEQ ID (13)
W213	Artificial or Unknown found in <213> in SEQ ID (14)
W213	Artificial or Unknown found in <213> in SEQ ID (15)

The warnings shown above are ok and require no response.

\*\*\*\*\*

Application No: 10583415 Version No: 2.0

Input Set:

Output Set:

**Started:** 2009-06-24 14:16:41.386  
**Finished:** 2009-06-24 14:16:43.604  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 218 ms  
**Total Warnings:** 15  
**Total Errors:** 8  
**No. of SeqIDs Defined:** 15  
**Actual SeqID Count:** 15

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 9 )
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 10 )
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 11 )
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 12 )
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 13 )

**Input Set:**

**Output Set:**

**Started:** 2009-06-24 14:16:41.386  
**Finished:** 2009-06-24 14:16:43.604  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 218 ms  
**Total Warnings:** 15  
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**No. of SeqIDs Defined:** 15  
**Actual SeqID Count:** 15

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 14 )
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID ( 15 )
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 250	Structural Validation Error; Sequence listing may not be indexable

# SEQUENCE LISTING

<110> MEYER, ROMAN  
 SCHUTZ, MICHAEL  
 GRALLERT, HOLGER  
 GRASSL, RENATE  
 MILLER, STEFAN

<120> ENDOTOXIN DETECTION METHOD

<130> DEBE:067US

<140> 10/583,415

<141> 2006-06-15

<150> PCT/DE2004/002778

<151> 2004-12-20

<150> DE 103 60 844.3

<151> 2003-12-20

<160> 15

<170> PatentIn version 3.3

<210> 1

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 1

gaaggaacta gtcatatggc tagctggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggt 78

<210> 2

<211> 54

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 2

acgcgcgcaaag cttgtcgacg gatcctatca ttcttttacc ttaattatgt agtt 54

<210> 3

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 3

gaaggaacta gtcatatggc ttgttggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggt 78

<210> 4

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 4

gaaggaacta gtcatatggc tagctggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggt 78

<210> 5

<211> 19

<212> PRT

<213> artificial sequence

<220>

<223> strep tag

<400> 5

Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn

1 5 10 15

Thr Tyr Gln

<210> 6

<211> 19

<212> PRT

<213> artificial sequence

<220>

<223> strep tag

<400> 6

Met Ala Cys Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn

1 5 10 15

Thr Tyr Gln

<210> 7  
<211> 19  
<212> PRT  
<213> artificial sequence

<220>  
<223> strep tag

<400> 7

Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Cys Asn Asn  
1 5 10 15

Thr Tyr Gln

<210> 8  
<211> 539  
<212> PRT  
<213> artificial sequence

<220>  
<223> T4p12 with strep tag

<400> 8

Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn  
1 5 10 15

Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val Lys Phe Asp Pro  
20 25 30

Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val Gln Ala Ala Ile  
35 40 45

Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro Asp Ala Ser Ser  
50 55 60

Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln Glu Val Ile Asp  
65 70 75 80

Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr Leu Ala Thr Arg  
85 90 95

Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly Leu Thr Arg Tyr  
100 105 110

Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn Glu Ser Ser Ile  
115 120 125

Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val Phe Glu Thr Arg  
130 135 140

Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile Ser Ser Leu Pro  
145 150 155 160

Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met Thr Pro Leu Lys  
165 170 175

Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile Ala Pro Ser Lys  
180 185 190

Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln Leu Ala Thr Val  
195 200 205

Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr Ala Ile Ser Pro  
210 215 220

Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr Lys Gly Val Ile  
225 230 235 240

Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn Ala Ser Val Ala  
245 250 255

Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr Thr Ser Met Arg  
260 265 270

Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln Ser Gly Gly Asp  
275 280 285

Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile His Gln Arg Gly  
290 295 300

Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn Thr Leu Thr Ile  
305 310 315 320

Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn Met Thr Gly Gly  
325 330 335

Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu Ile Asp Arg Thr



340

345

350

Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp Ser Leu Pro Ser  
 355 360 365

Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser Ala Ser Asp Cys  
 370 375 380

Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly Gly Ser Ser Ser  
 385 390 395 400

Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val Arg Gly Ser Gly  
 405 410 415

Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly Asn Asp Gln Phe  
 420 425 430

Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly Tyr Val Gly Glu  
 435 440 445

Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala Gly Gly Phe Gly  
 450 455 460

Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg Arg Ser Asn Phe  
 465 470 475 480

Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg Ser Tyr Phe Thr  
 485 490 495

Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg Asn Ser Arg Tyr  
 500 505 510

Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr Arg Pro Trp Asn  
 515 520 525

Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu  
 530 535

&lt;210&gt; 9

&lt;211&gt; 527

&lt;213&gt; unknown

&lt;220&gt;

&lt;223&gt; protein p12 of T2 phage

<400> 9

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val  
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val  
20 25 30

Gln Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro  
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln  
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr  
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly  
85 90 95

Leu Thr Arg Tyr Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn  
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val  
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile  
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met  
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile  
165 170 175

Ala Pro Ser Lys Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln  
180 185 190

Leu Ala Thr Val Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr  
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr  
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn  
225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr  
245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln  
260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile  
275 280 285

His Gln Arg Gly Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn  
290 295 300

Thr Leu Thr Ile Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn  
305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu  
325 330 335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp  
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser  
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly  
370 375 380

Gly Thr Ser Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val  
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly  
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly  
420 425 430

Tyr Val Gly Glu Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala  
435 440 445

Gly Gly Phe Gly Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg  
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg  
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg  
485 490 495

Asn Ser Arg Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr  
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu  
515 520 525

<210> 10

<211> 527

<213> unknown

<220>

<223> protein p12 of T4 phage

<400> 10

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val  
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val  
20 25 30

His Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro  
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Ile Pro Thr Glu Gln  
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr  
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Thr Val Tyr Gly  
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Asp Glu Ala Ile Ala Gly Val Asn Asn  
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Ala		
115	120	125
Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile		
130	135	140
Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met		
145	150	155 160
Thr Pro Leu Lys Thr Gln Gln Leu Ala Ile Lys Leu Ile Ala Gln Ile		
165	170	175
Ala Pro Ser Glu Thr Thr Ala Thr Glu Ser Asp Gln Gly Val Val Gln		
180	185	190
Leu Ala Thr Val Ala Gln Val Arg Gln Gly Thr Leu Arg Glu Gly Tyr		
195	200	205
Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Ser Ser Thr Glu Glu Tyr		
210	215	220
Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn		
225	230	235 240
Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr		
245	250	255
Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln		
260	265	270
Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile		
275	280	285
Gln Gln Arg Gly Gly Gln Ile Ile Tyr Gly Thr Leu Arg Ile Glu Asp		
290	295	300
Thr Phe Thr Ile Ala Asn Gly Gly Ala Asn Ile Thr Gly Thr Val Arg		
305	310	315 320
Met Thr Gly Gly Tyr Ile Gln Gly Asn Arg Ile Val Thr Gln Asn Glu		
325	330	335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp  
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser  
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly  
370 375 380

Gly Asn Pro Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val  
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly  
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly  
420 425 430

Tyr Val Gly Glu Val Gln Ile Gln Gln Met Ser Tyr His Lys His Ala  
435 440 445

Gly Gly Phe Gly Glu His Asp Asp Leu Gly Ala Phe Gly Asn Thr Arg  
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg  
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Glu Ser Gln Arg  
485 490 495

Asn Ser Lys Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr  
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu  
515 520 525

<210> 11

<211> 518

<213> unknown

<220>

<223> protein p12 of PP01 phage

<400> 11

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Lys Tyr Val  
1 5 10 15

Lys Phe Asp Pro Val Gly Ser Asn Phe Pro Asp Thr Val Thr Thr Val  
20 25 30

Gln Ser Ala Leu Ser Lys Ile Ser Asn Ile Gly Val Asn Gly Ile Pro  
35 40 45

Asp Ala Ser Met Glu Val Lys Gly Ile Ala Met Ile Ala Ser Glu Gln  
50 55 60

Glu Val Leu Asp Gly Thr Asn Asn Ser Lys Ile Val Thr Pro Ala Thr  
65 70 75 80

Leu Ala Thr Arg Leu Leu Tyr Pro Asn Ala Thr Glu Thr Lys Tyr Gly  
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Glu Glu Thr Leu Glu Gly Ser Asp Asn  
100 105 110

Asn Ser Ser Ile Thr Pro Gln Lys Leu Lys Tyr His Thr Asp Asp Val  
115 120 125

Phe Gln Asn Arg Tyr Ser Ser Glu Ser Ser Asn Gly Val Ile Lys Ile  
130 135 140

Ser Ser Thr Pro Ala Ala Leu Ala Gly Val Asp Asp Thr Thr Ala Met  
145 150 155 160

Thr Pro Leu Lys Thr Gln Lys Leu Ala Ile Lys Leu Ile Ser Gln Ile  
165 170 175

Ala Pro Ser Glu Asp Thr Ala Ser Glu Ser Val Arg Gly Val Val Gln  
180 185 190

Leu Ser Thr Val Ala Gln Thr Arg Gln Gly Thr Leu Arg Glu Gly Tyr  
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Val Ala Thr Gln Glu Tyr  
210 215 220

Lys Gly Val Ile Arg Leu Gly Thr Gln Ser Glu Ile Asn Ser Asn Leu

225

230

235

240

Gly Asp Val Ala Val Thr Gly Glu Thr Leu Asn Gly Arg Gly Ala Thr  
245 250 255

Gly Ser Met Arg Gly Val Val Lys Leu Thr Thr Gln Ala Gly Ile Ala  
260 265 270